

**BLAST2 Search Results****EXHIBIT B**Docket No.: PF-0609 USN  
USSN: 09/806,267[Sequences](#) [Help](#)[Retrieval](#) [BLAST2](#) [FASTA](#) [ClustalW](#) [CCG Assembly](#) [Phrap](#) [Translation](#)  
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**Program: blastp****Sequence ID(s):**☐ 135698CD1 vs. genpept137

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 135698CD1  
(234 letters)Database: genpept137  
1,534,369 sequences; 474,463,515 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
<input checked="" type="checkbox"/> <u>g27728685</u> anti-rabies SOJA immunoglobulin kappa light chain [	444	e-124
<input checked="" type="checkbox"/> <u>g21619606</u> similar to anti TNF-alpha antibody light-chain Fab	436	e-121
<input checked="" type="checkbox"/> <u>g17645754</u> unnamed protein product [Homo sapiens]	434	e-121
<input checked="" type="checkbox"/> <u>g17644683</u> unnamed protein product [Homo sapiens]	434	e-121
<input checked="" type="checkbox"/> <u>g21410096</u> Unknown (protein for MGC:22645) [Homo sapiens]	431	e-119
<input checked="" type="checkbox"/> <u>g17645758</u> unnamed protein product [Homo sapiens]	430	e-119
<input checked="" type="checkbox"/> <u>g17644687</u> unnamed protein product [Homo sapiens]	430	e-119
<input checked="" type="checkbox"/> <u>g16741061</u> Similar to immunoglobulin kappa constant [Homo sapiens]	430	e-119
<input checked="" type="checkbox"/> <u>g23683336</u> immunoglobulin kappa light chain [Homo sapiens]	423	e-117
<input checked="" type="checkbox"/> <u>g21669465</u> immunoglobulin kappa light chain VLJ region [Homo sapiens]	415	e-115

>g27728685 anti-rabies SOJA immunoglobulin kappa light chain [Homo sapiens]  
Length = 234

Score = 444 bits (1131), Expect = e-124  
Identities = 217/234 (92%), Positives = 224/234 (94%)

Query: 1 MEAPAQLLFLLLLWLPD'TTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKP 60  
MEAPAQLLFLLLLWLPD'TTGEIVLTQSPATLSLSPGERATL+CRASQ+ S YLAWYQQKP  
Sbjct: 1 MEAPAQLLFLLLLWLPD'TTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP 60

Query: 61 GQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTTPYTFGQ 120  
GQAPRLLIYD SNRATGIP RFSGSGSGTDFTLT+IS LEPED A+YYCQQ F P+TFGQ  
Sbjct: 61 GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLTSSISLEPEDFAVYYCQQRFNWPWTFGQ 120

Query: 121 GTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180  
GT++E KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ  
Sbjct: 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180

Query: 181 ESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
ESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC  
Sbjct: 181 ESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234

>g21619606 similar to anti TNF-alpha antibody light-chain Fab  
fragment [Homo sapiens]  
Length = 236

Score = 436 bits (1110), Expect = e-121  
Identities = 219/236 (92%), Positives = 225/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD'TTGEIVLTQSPATLSLSPGERATLSCRASQSVSS-YLAWYQQK 59  
ME PAQLLFLLLLWLPD+TGE VLTQSP TSLSPGERATLSCRASQS+SS YLAWYQQK  
Sbjct: 1 METPAQLLFLLLLWLPDSTGENVLTQSPGTLSPGERATLSCRASQSLSSSYLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTT-PYTF 118  
PGQAPRLLIY S+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQY T+ P TF  
Sbjct: 61 PGQAPRLLIYGSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSRPITF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178  
GQGTRL+IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN  
Sbjct: 121 GQGTRLDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
SQESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC  
Sbjct: 181 SQESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g17645754 unnamed protein product [Homo sapiens]  
Length = 236

Score = 434 bits (1105), Expect = e-121  
Identities = 217/236 (91%), Positives = 226/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD'TTGEIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQK 59  
ME PAQLLFLLLLWLPD'TTGEIVLTQSP TSLSPGERATLSCRASQ++ SSYLAWYQQK  
Sbjct: 1 METPAQLLFLLLLWLPD'TTGEIVLTQSPGTLSPGERATLSCRASQNIRSSYLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTTPY-TF 118  
PGQAP LLIY AS+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQ+ ++P +F  
Sbjct: 61 PGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178  
GQGT+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN  
Sbjct: 121 GQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
SQESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC  
Sbjct: 181 SQESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g17644683 unnamed protein product [Homo sapiens]

Length = 236

Score = 434 bits (1105), Expect = e-121

Identities = 217/236 (91%), Positives = 226/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQK 59  
ME PAQLLFLLLLWLPD TTGEIVLTQSP TSLSPGERATLSCRASQ++ SSYLAWYQQK  
Sbjct: 1 METPAQLLFLLLLWLPD TTGEIVLTQSPG TSLSPGERATLSCRASQNIRSSYLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPY-TF 118  
PGQAP LLIY AS+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQ+ ++P +F  
Sbjct: 61 PGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMC SF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178  
GQGT+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN  
Sbjct: 121 GQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 234  
SQESVTEQDSKDYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC  
Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 236

>g21410096 Unknown (protein for MGC:22645) [Homo sapiens]  
Length = 234

Score = 431 bits (1096), Expect = e-119

Identities = 210/234 (89%), Positives = 224/234 (94%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKP 60  
MEAPAQLLFLLLLWLPD TTGEIV+TQSPATLS+SPGERATLSCRASQSV+S LAWYQQ P  
Sbjct: 1 MEAPAQLLFLLLLWLPD TTGEIVMTQSPATLSVSPGERATLSCRASQSVTSNLAWYQQTP 60

Query: 61 GQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPYTFGQ 120  
GQ+PRL+IY AS+RA+G+P RFSGSGSGT+FTLTIS L+ ED A+YYCQQY P+TFGQ  
Sbjct: 61 GQSPRLVIYGASSRASGV PARFSGSGSGTEFTLTISLQSEDFAVYYCQQYNKWPHTFGQ 120

Query: 121 GTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180  
GT+L+IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ  
Sbjct: 121 GTKLDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180

Query: 181 ESVTEQDSKDYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 234  
ESVTEQDSKDYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC  
Sbjct: 181 ESVTEQDSKDYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 234

>g17645758 unnamed protein product [Homo sapiens]  
Length = 236

Score = 430 bits (1095), Expect = e-119

Identities = 216/236 (91%), Positives = 225/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSSY-LAWYQQK 59  
ME PAQLLFLLLLWLPD TTGEIVLTQSP TSLSPGERATLSCRASQS+SS LAWYQQK  
Sbjct: 1 METPAQLLFLLLLWLPD TTGEIVLTQSPG TSLSPGERATLSCRASQSISSSSLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPY-TF 118  
PGQAP LLI+ AS+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQ+ ++P +F  
Sbjct: 61 PGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMC SF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178  
GQGT+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN  
Sbjct: 121 GQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 234  
SQESVTEQDSKDYSLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC

Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g17644687 unnamed protein product [Homo sapiens]  
Length = 236

Score = 430 bits (1095), Expect = e-119  
Identities = 216/236 (91%), Positives = 225/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSSY-LAWYQQK 59  
ME PAQLLFLLLLWLPD TTGEIVLTQSP TLSPGERATLSCRASQS+SS LAWYQQK  
Sbjct: 1 METPAQLLFLLLLWLPD TTGEIVLTQSPGTLSPGERATLSCRASQSISSSLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPY-TF 118  
PGQAP LLI+ AS+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQ+ ++P +F  
Sbjct: 61 PGQAPGLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178  
GQGT+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN  
Sbjct: 121 GQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC  
Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g16741061 Similar to immunoglobulin kappa constant [Homo sapiens]  
Length = 235

Score = 430 bits (1095), Expect = e-119  
Identities = 214/235 (91%), Positives = 224/235 (95%), Gaps = 1/235 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSS-YLAWYQQK 59  
ME PAQLLFLLLLWLP TTGEIVLTQSPATLSLSPGERATLSCRASQ VSS YLAWYQQK  
Sbjct: 1 METPAQLLFLLLLWLP GTTGEIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPYTFG 119  
PGQAPRL++ +S+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQY ++ TFG  
Sbjct: 61 PGQAPRLLMFGSSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSQGTFG 120

Query: 120 QGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 179  
GT+++IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS  
Sbjct: 121 PGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 180

Query: 180 QESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
QESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC  
Sbjct: 181 QESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

>g23683336 immunoglobulin kappa light chain [Homo sapiens]  
Length = 236

Score = 423 bits (1077), Expect = e-117  
Identities = 213/236 (90%), Positives = 220/236 (92%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLP--DTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ 58  
ME PAQLLFLLLLWLP DTTGEIV+TQSPATLS+SPGERATLSCRASQSV S LAWYQQ  
Sbjct: 1 METPAQLLFLLLLWLPVSDTTGEIVMTQSPATLSVSPGERATLSCRASQSVRSNLAWYQQ 60

Query: 59 KPGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPYTF 118  
KPGQAPRLLIY AS RATGIP RFSGSGSGT+FTLTIS L+ ED A+YYCQQY TF  
Sbjct: 61 KPGQAPRLLIYA ASTRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYNEWFRFTF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178  
GQGT++EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN

Sbjct: 121 GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g21669465 immunoglobulin kappa light chain VLJ region [Homo  
sapiens]  
Length = 265

Score = 415 bits (1055), Expect = e-115

Identities = 209/232 (90%), Positives = 213/232 (91%), Gaps = 1/232 (0%)

Query: 4 PAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQA 63  
P LLLL E LTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQA

Sbjct: 6 PTAAAGLLLLAAQPMAAETTLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQA 65

Query: 64 PRLLIYDASNRATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTP-YTFGQGT 122  
PRLLIYDASNRATGIP RFGSGSGSGTDFTLTISRLEPED A+YYCQQY ++P YTFGQGT

Sbjct: 66 PRLLIYDASNRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGT 125

Query: 123 RLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES 182  
+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES

Sbjct: 126 KLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES 185

Query: 183 VTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
VTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Sbjct: 186 VTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

Database: genpept137

Posted date: Sep 11, 2003 11:22 AM

Number of letters in database: 474,463,515

Number of sequences in database: 1,534,369

Lambda	K	H
0.314	0.129	0.377

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 225373096

Number of Sequences: 1534369

Number of extensions: 8964668

Number of successful extensions: 79945

Number of sequences better than 10.0: 32966

Number of HSP's better than 10.0 without gapping: 14318

Number of HSP's successfully gapped in prelim test: 18648

Number of HSP's that attempted gapping in prelim test: 44709

Number of HSP's gapped (non-prelim): 35882

length of query: 234

length of database: 474,463,515

effective HSP length: 60

effective length of query: 174

effective length of database: 382,401,375

effective search space: 66537839250

effective search space used: 66537839250

T: 11

A: 40

X1: 16 ( 7.2 bits)

X2: 38 (14.8 bits)  
X3: 64 (24.9 bits)  
S1: 42 (22.0 bits)

[Graphical Viewer...](#)

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Submit sequences to:

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